

Hum: 1 MATAGGSGADPGSRGLRLLSFCVLLAGLCRGNVSVERKIYIPLNKTAPCVRLLNATHQI 60
Mou MAT GGSG DPGSRGLL LLSF V+LAGLC GNSVERKIYIPLNKTAPCVRLLNATHQI
Dros: 1 A + +G K+Y P+ A C R LN THQ
C.ele L +++AG+C G S + + + + C R N TH+

Hum 61 GCQSSISGDTGVIHVVEKEEDLQWLTGDNPPYMLLESKHFTDRDLMEKLGKRTSRIAG 120
Mou GCQSSISGDTGVIHVVEKEEDL+WLTGDNPPYMLLE K FTRD+MEKLG TSRIAG
Dros GC S+ SG GV+H++ E DL++L+ P+PPY ++ FTR+ + +LK +
C.eleg GCQ++ + G+I ++K+ED + W + Y LL RD + +LK + ++G

Hum: 121 LAVSLTKPSPASGFSPSVQCPNDGFGVYSNSYGPFAHCHREIQWNSLGNLAYEDFSFPI 180
Mou LAV+L KP+ S FSPSVQCPNDGFG YSNSYGPEFAH ++ WN LG GLAYED SFPI
Dros + + + + + FS + CPN G+ S S + + + + WN G GL +EDF FPI
C.eleg + +S + + + S +CPN Y E+ E + NS G+GL D+ +

Hum: 181 FLEDENETKVIKQCYQDHNLSQNGSAPTFFPLCAMQLFSHMAVISTATCMRRSSIQSTF 240
Mou FLEDE+ETKVIKQCYQDHNL QNGSAP+FPPLCAMQLFSHMAVISTATCMRRS IQSTF
Dros: + + D ++ +++C+QD N + LCA+++ S M A ++T CMRR++ +
C.eleg +++ + ++I++CY N + + +P C M A ++ C RR + F

Hum: 241 SINPEIVCDPLSDYNVWSMLKPINTTGLKPDPRVVVAATPLDSRFF-WNVAPGAESAV 299
Mous SINPEIVCDPLSDYNVWSMLKPINT+ L+PD RVVVAATPLDSRFF WNVAPG ESAV
Dros ++ CDPL NV P +T T+ +++ ++ RLD+ + F V GA ++
C.eleg +N + +C + N+++ PI T+ T+ + ++ R+DS ++ G S +

Hum: 300 ASFVTQLAAAEALQKAPDVTTLPRNVMFVFFQGETFDYIGSSRMVYDMEKGFPVQLENV 359
Mou ASFVTQLAAAEAL KAPDVTTL.RNVMFVFFQGETFDYIGSSRMVYDME KGFPV+LEN+
Dros F A LQ P + NV+V F GE++DYIGS R VYDMEK +Fp+ +N+
C.eleg S ++ LAAA ++/QKA + + RNV F FF GE+ DYIGS Y ME KGFP++ +

Figure 1A

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Hum: 360 DSFVELGQVALRTSLWMHTDPVSQKNESVRNQVEDLLATLEKSGAGVPAVILRRPNQS 419
Mou DSFVELGQVALRTSL+LWMHTDP+SQKNESV+NQVEDLLATLEKSGAGVP V+LRR QS
Dros D +++G + +++L + ++ Q+ + L KS G I + S
C.eleg D +E+ Q+ + + ++H D ++ + + Q + ++ +E+ G A L +P+ S

Hum 420 QPLPPSSLQRFRLARNISGVVLADHSGAFHNKYQSIYDTAENINVSYPEWLSPEEDLNF 479
Mou Q PPSSLQRFRLARNISGVVLADHSG+FNH+YQSIYDTAENINVSYPEW S EEDLNF
Dros LPP+S Q FLR N + ++L + NKYY S YD A+N++ +Y L
C.eleg +PP+S F +A ++ V+LA + + + S+ D EW E +

Hum 480 VDTAKALADVATVLCRALYELAGGTNFSDTVQADPQTVTRLLYGFLIKANNWFQSIILR 539
Mous VDTAKALA+VATVL RALYELAGGTNFS ++QADPQTVTRLLYGFL++ANNWFQSIIL+
Dros V D DV++++ ALY+ G ++ T A+P LY FL A+ F++
C.eleg + + V+T + A + G + D + +T ++ LI +N WF

Hum : 540 QDLRSYLGDPLOHYIAVSSPTNTTYVQYALANLTGTVVNLTREQCQDPKVPSENKDL 599
Mous DLSRYL D PLQHYIAVSSPTNTTYVQYAL NLTG NLTREQCQDPKVP+E+KDL
Dros S L + P YI+V + + Y L L+ ++ R+ C D
C.eleg Q L SY G YI++ SPT ++ +AL + T+ + + C + + +

Hum: 600 YEYSWVQGPLHSNETDRLPRCVRSTARLARALSPAFELSQWSSSTEYSTWESRWKDIRAR 659
Mous YEYSWVQGP +SN T+RLP+CVRST RLARALSPAFELSQWSSSTEYSTW ESRWKDI+AR
Dros PLH + + C +T + +LSPAF + WSS YSTWES W AR
C.eleg Y Y+W P N + C++S +SPA + + +T YSTW ES +

Hum: 660 IFLIASKELELITLTVGFGILIFSLIVTYCINAKADVLF+APREPGAVSY 709
Mous IFLIASKELE ITL VGF L+FSLIVTYCINAKADVLF+APREPGAVSY
Dros IFL S ++ TL+VG +LI S + Y I+++++VLF
C.eleg ++L+ E + + +I +L+ + + ++ FI EP A

Figure 1B